

b) combining said biological sample with said [nucleotide] oligonucleotide or polynucleotide under conditions such that a hybridization complex is formed between [said nucleic acid and said nucleotide] the nucleic acid in said biological sample and oligonucleotide or polynucleotide; and

c) detecting said hybridization complex.

9. (Amended) The method of Claim 8, wherein, said nucleic acid [corresponding to the nucleotide sequence of SEQ ID NO:100] encoding a human telomerase polypeptide is a ribonucleic acid.

11. (Amended) The method of Claim 8, wherein, said nucleic acid [corresponding to the nucleotide sequence of SEQ ID NO:100] encoding a human telomerase polypeptide is a deoxyribonucleic acid.

12. (Amended) The method of Claim 11, wherein said detecting of said hybridization complex comprises conditions that permit the detection of [alterations in the nucleotide of] a deletion, insertion, or point mutation in the sequence of the nucleic acid encoding a human telomerase polypeptide when compared to SEQ ID NO:100 [in said biological sample].

Please add the following new claims:

--21. A method of detecting the presence of an nucleic acid that encodes a telomerase protein in a sample comprising:

a) contacting the sample with a oligonucleotide or polynucleotide that specifically hybridizes to said nucleic acid, and detecting the hybridization complex; or,

b) amplifying said nucleic acid and detecting the amplification product; wherein the nucleic acid hybridizes under stringent conditions to a polynucleotide identical or complementary to SEQ ID NO:100.

22. The method of claim 21, wherein the sample is from a human tissue sample.

23. The method of claim 21 wherein the amplification is carried out using a polymerase chain reaction method.
24. A method for diagnosing a telomerase-related condition in a patient, comprising:
 - a) obtaining a cell or tissue sample from the patient;
 - b) determining an amount of an RNA encoding a human telomerase protein hTRT gene product in the cell or tissue by:
 - 1) contacting the sample with a nucleic acid that specifically hybridizes to said RNA, and detecting the hybridization complex; or,
 - 2) amplifying said RNA and detecting the amplification product; wherein the RNA hybridizes under stringent conditions to a polynucleotide having a sequence exactly complementary to SEQ ID NO:100; and,
 - c) comparing the amount of hTRT gene product in the cell or tissue determined in step (b) with the amount in a cell or tissue sample of the same type from a healthy subject,
25. An isolated or purified polynucleotide having a sequence of SEQ ID NO:100, wherein said polynucleotide is from about 10 nucleotides to about 2171 nucleotides in length.
26. A polypeptide encoded by the polynucleotide of claim 25.

REMARKS

Following entry of this Amendment, claims 1-26 will be pending. Support for this Amendment is replete in the specification. For example, the "deletion, insertion, or point mutations" referred to in claim 12 find support in the specification at, e.g., page 26, lines 15-25. Stringent hybridization (e.g., claim 21) is described in the specification at, e.g., page 23, line 24 to page 24, line 10. Amplification of nucleic acid sequences (e.g., claims 21 and 23) is described in the specification at, e.g., page 20, line 24 to page 22, line 5. Descriptions of the detection of